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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=20; hr=16; min=33; sec=18; ms=784;]

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Output Set:

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Started:      2008-05-02 14:58:00.513
Finished:    2008-05-02 14:58:06.479
Elapsed:     0 hr(s) 0 min(s) 5 sec(s) 966 ms
Total Warnings: 77
Total Errors:  42
No. of SeqIDs Defined: 89
Actual SeqID Count: 89

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[illegible]

Input Set:

Output Set:

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Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
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W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> JONSON, LARS
 REHFELD, JENS F.
 JOHNSEN, ANDERS H.

<120> METHODS FOR INCREASING THE PRODUCTION OF A
 RECOMBINANT POLYPEPTIDE FROM A HOST CELL

<130> 030307-0256

<140> 10528563

<141> 2005-10-11

<150> PCT/DK03/00609

<151> 2003-09-19

<150> DK PA200201391

<151> 2002-09-20

<160> 89

<170> PatentIn Ver. 3.3

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Pitrilysin
 consensus sequence

<220>

<221> MOD_RES

<222> (2)..(3)

<223> Variable amino acid

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<210> 2

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pitrilysin
 consensus sequence

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<223> Variable amino acid

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<220>
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<222> (14)..(35)
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<222> (36)..(37)
<223> Variable amino acid or absent

<220>
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<222> (40)
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<220>
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<222> (42)..(45)
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1 5 10 15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
20 25 30
Xaa Xaa Xaa Xaa Xaa Asn Ala Xaa Thr Xaa Xaa Xaa Xaa Thr
35 40 45

<210> 3
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pitrilysin
consensus sequence

<220>
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Tyr Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Asn Ala Xaa Thr Xaa Xaa Xaa Xaa Xaa Thr
 35 40 45

<210> 4
 <211> 989
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 4

Met Leu Arg Phe Gln Arg Phe Ala Ser Ser Tyr Ala Gln Ala Gln Ala
 1 5 10 15

Val Arg Lys Tyr Pro Val Gly Gly Ile Phe His Gly Tyr Glu Val Arg
 20 25 30

Arg Ile Leu Pro Val Pro Glu Leu Arg Leu Thr Ala Val Asp Leu Val
 35 40 45

His Ser Gln Thr Gly Ala Glu His Leu His Ile Asp Arg Asp Asp Lys
 50 55 60

Asn Asn Val Phe Ser Ile Ala Phe Lys Thr Asn Pro Pro Asp Ser Thr
 65 70 75 80

Gly Val Pro His Ile Leu Glu His Thr Thr Leu Cys Gly Ser Val Lys
 85 90 95

Tyr Pro Val Arg Asp Pro Phe Phe Lys Met Leu Asn Lys Ser Leu Ala
 100 105 110

Asn Phe Met Asn Ala Met Thr Gly Pro Asp Tyr Thr Phe Phe Pro Phe
 115 120 125

Ser Thr Thr Asn Pro Gln Asp Phe Ala Asn Leu Arg Gly Val Tyr Leu
 130 135 140

Asp Ser Thr Leu Asn Pro Leu Leu Lys Gln Glu Asp Phe Asp Gln Glu
 145 150 155 160

Gly Trp Arg Leu Glu His Lys Asn Ile Thr Asp Pro Glu Ser Asn Ile
 165 170 175

Val Phe Lys Gly Val Val Tyr Asn Glu Met Lys Gly Gln Ile Ser Asn
 180 185 190

Ala Asn Tyr Tyr Phe Trp Ser Lys Phe Gln Gln Ser Ile Tyr Pro Ser
 195 200 205

Leu Asn Asn Ser Gly Gly Asp Pro Met Lys Ile Thr Asp Leu Arg Tyr
 210 215 220

Gly Asp Leu Leu Asp Phe His His Lys Asn Tyr His Pro Ser Asn Ala

225		230		235		240
Lys Thr Phe Thr Tyr Gly Asn Leu Pro Leu Val Asp Thr Leu Lys Gln						
	245		250		255	
Leu Asn Glu Gln Phe Ser Gly Tyr Gly Lys Arg Ala Arg Lys Asp Lys						
	260		265		270	
Leu Leu Met Pro Ile Asp Leu Lys Lys Asp Ile Asp Val Lys Leu Leu						
	275		280		285	
Gly Gln Ile Asp Thr Met Leu Pro Pro Glu Lys Gln Thr Lys Ala Ser						
	290		295		300	
Met Thr Trp Ile Cys Gly Ala Pro Gln Asp Thr Tyr Asp Thr Phe Leu						
	305		310		315	
Leu Lys Val Leu Gly Asn Leu Leu Met Asp Gly His Ser Ser Val Met						
	325		330		335	
Tyr Gln Lys Leu Ile Glu Ser Gly Ile Gly Leu Glu Phe Ser Val Asn						
	340		345		350	
Ser Gly Val Glu Pro Thr Thr Ala Val Asn Leu Leu Thr Val Gly Ile						
	355		360		365	
Gln Gly Val Ser Asp Ile Glu Ile Phe Lys Asp Thr Val Asn Asn Ile						
	370		375		380	
Phe Gln Asn Leu Leu Glu Thr Glu His Pro Phe Asp Arg Lys Arg Ile						
	385		390		395	
Asp Ala Ile Ile Glu Gln Leu Glu Leu Ser Lys Lys Asp Gln Lys Ala						
	405		410		415	
Asp Phe Gly Leu Gln Leu Leu Tyr Ser Ile Leu Pro Gly Trp Thr Asn						
	420		425		430	
Lys Ile Asp Pro Phe Glu Ser Leu Leu Phe Glu Asp Val Leu Gln Arg						
	435		440		445	
Phe Arg Gly Asp Leu Glu Thr Lys Gly Asp Thr Leu Phe Gln Asp Leu						
	450		455		460	
Ile Arg Lys Tyr Ile Val His Lys Pro Cys Phe Thr Phe Ser Ile Gln						
	465		470		475	
Gly Ser Glu Glu Phe Ser Lys Ser Leu Asp Asp Glu Glu Gln Thr Arg						
	485		490		495	
Leu Arg Glu Lys Ile Thr Ala Leu Asp Glu Gln Asp Lys Lys Asn Ile						
	500		505		510	
Phe Lys Arg Gly Ile Leu Leu Gln Glu Lys Gln Asn Glu Lys Glu Asp						
	515		520		525	
Leu Ser Cys Leu Pro Thr Leu Gln Ile Lys Asp Ile Pro Arg Ala Gly						

530		535		540	
Asp Lys Tyr Ser Ile Glu Gln Lys Asn Asn Thr Met Ser Arg Ile Thr					
545		550		555	560
Asp Thr Asn Gly Ile Thr Tyr Val Arg Gly Lys Arg Leu Leu Asn Asp					
	565		570		575
Ile Ile Pro Phe Glu Leu Phe Pro Tyr Leu Pro Leu Phe Ala Glu Ser					
	580		585		590
Leu Thr Asn Leu Gly Thr Thr Thr Glu Ser Phe Ser Glu Ile Glu Asp					
	595		600		605
Gln Ile Lys Leu His Thr Gly Gly Ile Ser Thr His Val Glu Val Thr					
	610		615		620
Ser Asp Pro Asn Thr Thr Glu Pro Arg Leu Ile Phe Gly Phe Asp Gly					
625		630		635	640
Trp Ser Leu Asn Ser Lys Thr Asp His Ile Phe Glu Phe Trp Ser Lys					
	645		650		655
Ile Leu Leu Glu Thr Asp Phe His Lys Asn Ser Asp Lys Leu Lys Val					
	660		665		670
Leu Ile Arg Leu Leu Ala Ser Ser Asn Thr Ser Ser Val Ala Asp Ala					
	675		680		685
Gly His Ala Phe Ala Arg Gly Tyr Ser Ala Ala His Tyr Arg Ser Ser					
	690		695		700
Gly Ala Ile Asn Glu Thr Leu Asn Gly Ile Glu Gln Leu Gln Phe Ile					
705		710		715	720
Asn Arg Leu His Ser Leu Leu Asp Asn Glu Glu Thr Phe Gln Arg Glu					
	725		730		735
Val Val Asp Lys Leu Thr Glu Leu Gln Lys Tyr Ile Val Asp Thr Asn					
	740		745		750
Asn Met Asn Phe Phe Ile Thr Ser Asp Ser Asp Val Gln Ala Lys Thr					
	755		760		765
Val Glu Ser Gln Ile Ser Lys Phe Met Glu Arg Leu Pro His Gly Ser					
	770		775		780
Cys Leu Pro Asn Gly Pro Lys Thr Ser Asp Tyr Pro Leu Ile Gly Ser					
785		790		795	800
Lys Cys Lys His Thr Leu Ile Lys Phe Pro Phe Gln Val His Tyr Thr					
	805		810		815
Ser Gln Ala Leu Leu Gly Val Pro Tyr Thr His Lys Asp Gly Ser Ala					
	820		825		830
Leu Gln Val Met Ser Asn Met Leu Thr Phe Lys His Leu His Arg Glu					

835

840

845

Val Arg Glu Lys Gly Gly Ala Tyr Gly Gly Gly Ala Ser Tyr Ser Ala
 850 855 860

Leu Ala Gly Ile Phe Ser Phe Tyr Ser Tyr Arg Asp Pro Gln Pro Leu
 865 870 875 880

Lys Ser Leu Glu Thr Phe Lys Asn Ser Gly Arg Tyr Ile Leu Asn Asp
 885 890 895

Ala Lys Trp Gly Val Thr Asp Leu Asp Glu Ala Lys Leu Thr Ile Phe
 900 905 910

Gln Gln Val Asp Ala Pro Lys Ser Pro Lys Gly Glu Gly Val Thr Tyr
 915 920 925

Phe Met Ser Gly Val Thr Asp Asp Met Lys Gln Ala Arg Arg Glu Gln
 930 935 940

Leu Leu Asp Val Ser Leu Leu Asp Val His Arg Val Ala Glu Lys Tyr
 945 950 955 960

Leu Leu Asn Lys Glu Gly Val Ser Thr Val Ile Gly Pro Gly Ile Glu
 965 970 975

Gly Lys Thr Val Ser Pro Asn Trp Glu Val Lys Glu Leu
 980 985

<210> 5

<211> 882

<212> PRT

<213> Schizosaccharomyces pombe

<400> 5

Met Asn Tyr Ala Lys Leu Ser Ile Ala Phe Ser Lys Lys Thr Ile Lys
 1 5 10 15

Thr His Asn Cys Arg Leu Phe Gln Arg Trp Leu His Val Gly Asp Lys
 20 25 30

Val His Asp Phe Arg Val Val Asp Thr Lys Lys Val Pro Glu Leu Gln
 35 40 45

Leu Asn Tyr Thr Arg Leu Lys His Glu Pro Thr Asn Ala Asp Met Ile
 50 55 60

His Leu Asp Arg Glu Asp Pro Asn Ser Val Phe Ser Ile Gly Phe Gln
 65 70 75 80

Thr Pro Ala Glu Asn Asp Glu Gly Ile Pro His Ile Leu Glu His Thr
 85 90 95

Thr Leu Cys Gly Ser Asn Lys Tyr Pro Val Arg Asp Pro Phe Phe Lys
 100 105 110

Met	Leu	Asn	Arg	Ser	Leu	Ala	Thr	Phe	Met	Asn	Ala	Phe	Thr	Ala	Ser	115	120	125	
Asp	Phe	Thr	Phe	Tyr	Pro	Phe	Ala	Thr	Val	Asn	Thr	Thr	Asp	Tyr	Lys	130	135	140	
Asn	Leu	Arg	Asp	Val	Tyr	Leu	Asp	Ala	Thr	Leu	Phe	Pro	Lys	Leu	Arg	145	150	155	160
Lys	Leu	Asp	Phe	Leu	Gln	Glu	Gly	Trp	Arg	Phe	Glu	His	Ala	Asp	Val	165	170	175	
Asn	Asp	Lys	Lys	Ser	Pro	Ile	Ile	Phe	Asn	Gly	Val	Val	Tyr	Asn	Glu	180	185	190	
Met	Lys	Gly	Gln	Val	Ser	Asp	Ser	Ser	Tyr	Ile	Phe	Tyr	Met	Leu	Phe	195	200	205	
Gln	Gln	His	Leu	Phe	Gln	Gly	Thr	Ala	Tyr	Gly	Phe	Asn	Ser	Gly	Gly	210	215	220	
Asp	Pro	Leu	Ala	Ile	Pro	Asp	Leu	Lys	Tyr	Glu	Glu	Leu	Val	Lys	Phe	225	230	235	240
His	Arg	Ser	His	Tyr	His	Pro	Ser	Asn	Ala	Lys	Ile	Leu	Ser	Tyr	Gly	245	250	255	
Ser	Phe	Pro	Leu	Glu	Asp	Asn	Leu	Ser	Ala	Leu	Ser	Glu	Thr	Phe	Arg	260	265	270	
Pro	Phe	Ser	Lys	Arg	Glu	Leu	Asn	Leu	Pro	Asn	Thr	Phe	Leu	Lys	Glu	275	280	285	
Phe	Asp	Gln	Glu	Lys	Arg	Val	Val	Glu	Tyr	Gly	Pro	Leu	Asp	Pro	Val	290	295	300	
Met	Ala	Pro	Gly	Arg	Gln	Val	Lys	Thr	Ser	Ile	Ser	Phe	Leu	Ala	Asn	305	310	315	320
Asp	Thr	Ser	Asn	Val	Tyr	Glu	Thr	Phe	Ala	Leu	Lys	Val	Leu	Ser	Lys	325	330	335	
Leu	Cys	Phe	Asp	Gly	Phe	Ser	Ser	Pro	Phe	Tyr	Lys	Ala	Leu	Ile	Glu	340	345	350	
Ser	Gly	Leu	Gly	Thr	Asp	Phe	Ala	Pro	Asn	Ser	Gly	Tyr	Asp	Ser	Thr	355	360	365	
Thr	Lys	Arg	Gly	Ile	Phe	Ser	Val	Gly	Leu	Glu	Gly	Ala	Ser	Glu	Glu	370	375	380	
Ser	Leu	Ala	Lys	Ile	Glu	Asn	Leu	Val	Tyr	Ser	Ile	Phe	Asn	Asp	Leu	385	390	395	400
Ala	Leu	Lys	Gly	Phe	Glu	Asn	Glu	Lys	Leu	Glu	Ala	Ile	Leu	His	Gln	405	410	415	

Met	Glu	Ile	Ser	Leu	Lys	His	Lys	Ser	Ala	His	Phe	Gly	Ile	Gly	Leu	420	425	430
Ala	Gln	Ser	Leu	Pro	Phe	Asn	Trp	Phe	Asn	Gly	Ala	Asp	Pro	Ala	Asp	435	440	445
Trp	Leu	Ser	Phe	Asn	Lys	Gln	Ile	Glu	Trp	Leu	Lys	Gln	Lys	Asn	Ser	450	455	460
Asp	Gly	Lys	Leu	Phe	Gln	Lys	Leu	Ile	Lys	Lys	Tyr	Ile	Leu	Glu	Asn	465	470	475
Lys	Ser	Arg	Phe	Val	Phe	Thr	Met	Leu	Pro	Ser	Ser	Thr	Phe	Pro	Gln	485	490	495
Arg	Leu	Gln	Glu	Ala	Glu	Ala	Lys	Lys	Leu	Gln	Glu	Arg	Thr	Ser	Lys	500	505	510
Leu	Thr	Asp	Glu	Asp	Ile	Ala	Glu	Ile	Glu	Lys	Thr	Ser	Val	Lys	Leu	515	520	525
Leu	Glu	Ala	Gln	Ser	Thr	Pro	Ala	Asp	Thr	Ser	Cys	Leu	Pro	Thr	Leu	530	535	540
Ser	Val	Ser	Asp	Ile	Pro	Glu	Thr	Ile	Asp	Glu	Thr	Lys	Leu	Lys	Phe	545	550	555
Leu	Asp	Ile	Ala	Gly	Met	Lys	Ala	Gln	Trp	Tyr	Asp	Leu	Ala	Ala	Gly	565	570	575
Leu	Thr	Tyr	Ile	Arg	Leu	Leu	Leu	Pro	Leu	Lys	Asn	Phe	Pro	Glu	Ser	580	585	590
Leu	Ile	Pro	Tyr	Leu	Pro	Val	Tyr	Cys	Asp	Ala	Cys	Leu	Asn	Leu	Gly	595	600	605
Thr	His	Ser	Glu	Ser	Ile	Gly	Asp	Leu	Glu	His	Gln	Ile	Arg	Arg	Tyr	610	615	620
Thr	Gly	Gly	Ile	Ser	Ile	Ser	Pro	Ser	Ala	Val	Thr	Asn	Asn	Ser	Asp	625	630	635
Val	Ser	Lys	Tyr	Glu	Leu	Gly	Ile	Ala	Ile	Ser	Gly	Tyr	Ala	Leu	Asp	645	650	655
Lys	Asn	Val	Gly	Lys	Leu	Val	Glu	Leu	Ile	Asn	Lys	Ala	Phe	Trp	Asn	660	665	670
Thr	Asn	Leu	Ser	Asn	Thr	Asp	Lys	Leu	Ala	Ile	Met	Leu	Lys	Thr	Ser	675	680	685
Val	Ser	Gly	Ile	Thr	Asp	Gly	Ile	Ala	Glu	Lys	Gly	His	Ser	Phe	Ala	690	695	700
Lys	Val	Ser	Ser	Ala	Ser	Gly	Leu	Thr	Glu	Lys	Thr	Ser	Ile	Thr	Glu	705	710	715
																		720

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725 730 735

Glu Glu Ser Phe Gly Pro Leu Val Glu Lys Leu Thr Ala Ile Arg Glu
740